

*From
Amendment*

FIGURE 1: ISS-pST gene construct

1 GCTAGCATGG CCCTGTGGAT GGCCTCCTG CCCCTGCTGG CGCTGCTGGC
5 51 CCTCTGGGA CCTGACCCAG CGCAGCCCT CGAGATGTTT CCAGCTATGC
101 CACTTCTTC TCTGTTCGCT AACGCTGTT TTCGGGCCA GCACCTGCAC
151 CAACTGGCTG CCGACACCTA CAAGGAGTTT GAGCGCCCT ACATCCCGA
201 GGGACAGAGG TACTCCATCC AGAACGCCA GGCTGCCCTC TGCTTCTCGG
251 AGACCATCCC GGCCCCACG GCAAGGACG AGGCCAGCA GAGATCGGAC
10 301 GTGGAGCTGC TGCGCTTCTC GCTGCTGCTC ATCCAGTCGT GGCTCGGGCC
351 CGTGCAGTTC CTCAGCAGGG TCTTCACCAA CAGCCTGGTG TTTGGCACCT
401 CAGACCGCGT CTACGAGAAG CTGAAGGACC TGGAGGAGGG CATCCAGGCC
451 CTGATGCGGG AGCTGGAGGA TGGCAGCCCC CGGGCAGGAC AGATCCTCAA
501 GCAAACCTAC GACAATTG ACACAAACTT GCGCAGTGAT GACGGCTGC
15 551 TTAAGAACTA CGGGCTGCTC TCCTGCTTCA AGAAGGACCT GCACAAGGCT
601 GAGACATACC TGCGGGTCAT GAAGTGTGCG CGCTTCGTGG AGAGCAGCTG
651 TGCCTTCTAG TCTAGA (SEQ ID NO:4)

20 ATG...GCC- insulin secretory signal.

GCTAGC- *Nhe* I restriction site incorporated into construct in order to ligate into plasmid.

CTCGAG- *Xho* I restriction site incorporated into construct in order to ligate secretory signal and pST.

25 TCTAGA- *Xba* I restriction site incorporated into construct in order to ligate into plasmid.

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FIGURE 2: ISS-pST peptide sequence.

1 MALWMRLPL LALLALWGPD PAAALEMFPA MPLSSLFANA VLRAQHLHQL
5 51 AADTYKEFER AYIPEGQRYS IQNAQAAFCF SETI PAPTGK DEAQQRSDVE
101 101 LLRFSLLLQ SWLGPVQFLS RVFTNSLVFG TSDRVYEKLK DLEEGIQALM
151 151 RELEDGSPPRA GQILKQTYDK FDTNLRSDA LLKNYGLLSC FKKDLHKAET
201 201 YLRVMKCRRF VESSCAF (SEQ ID NO: 3)

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MAL....AAA- insulin secretory signal, cleaved upon secretion of pST.

LE- function of XhoI cleavage site; result in no predicted secondary structural changes to pST.